

Isolation, taxonomy and ecophysiological characterization of endophytic fungi from *Ambrosia artemisiifolia*

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Ambrosia artemisiifolia (common ragweed) causes a serious health and environmental problems all over Hungary. Therefore the knowledge of its ecology, life-style and spreading is essential. Common ragweed can live with endophytic fungi in mutualistic relationship, without they causes negative symptoms to ragweed, although these fungi belong to plant pathogen genera such as *Alternaria*, *Fusarium*, *Mucor* and *Penicillium*. The advantage of them is that can help the host plant to uptake nutrients such as phosphorus and nitrogen, and secrete toxic alkaloids to protect the host plants against herbivores.

The goals of this research were to isolate and identify endophytic fungi from roots, stems and leaves of common ragweed deriving from typical sandy soil habitat types of Southern Great Hungarian Plain: grassland, field and abandoned field. Furthermore we described the most common endophytic fungal genera, which could help the life of the *Ambrosia* plants, from different habitats (field, abandoned field, lawn and roadsides). In addition we characterized the fungal isolates, measured their secreted enzymes: cellobiohydrolase, xylanase, β -1,3-glucanase, laccase, β -glucosidase, trypsin, chymotrypsin, cellulase, exochitinase, lipase and pectinase.

Endophytic fungi were isolated from symptomless *Ambrosia* roots, flowers and seeds from different habitats in Szolnok and near Maros in 2010, Kiskundorozsma and Ásotthalom in 2011. We made culturing from roots, leaves and flowers of common ragweed after surface sterilization and described the fungal colonies (105 colonies) at least in genus level. Most frequently *Penicillium*, *Mucor* and *Fusarium* species were isolated.

For the molecular identification, total DNA was extracted from the growing cultures belonging to distinct filamentous fungal genera. The fungal strains were identified by morphological characters and by ITS sequence analysis.

We sequenced the ITS region of 23 fungal strains from different genera and the following species were identified: *Absidia repens*, *Alternaria alternata*, *Fusarium chlamydosporum*, *Fusarium oxysporum*, *Fusarium redolens*, *Fusarium solani*, *Fusarium subglutinans*, *Meyerozyma guilliermondii*, *Mucor circinelloides*, *Penicillium aurantiogriseum*, *Pithomyces chartarum* - teleomorph: *Leptosphaerulina chartarum*.

In summary we can say that *Alternaria* and *Fusarium* species were the most abundant in flowers and seeds also, not only in the roots. *Alternaria* spores, linked to any part of the plant: adhered and germinated, could be seen by microscopical investigations. We identified *Alternaria* from *Ambrosia* seeds after aggressive surface sterilization, at first time. The activity of extracellular enzymes (laccase, cellobiohydrolase, exochitinase, β -1,3-glucanase, β -glucosidase, trypsin and lipase) activity of the fungal strains (*Alternaria*, *Fusarium*, *Penicillium* and *Mucor* genus) were also examined copper sulphate containing glucose minimal liquid medium. We experienced more increasing activity of enzyme activities in the case of the isolates belonging to the *Alternaria* and *Penicillium* genera. We ascertained that the endophytic fungal isolates could secrete cellobiohydrolase, xylanase, β -1,3-glucanase, laccase, β -glucosidase, trypsin, chymotrypsin, cellulase, exochitinase, lipase and pectinase enzymes.

Our data can contribute to more knowledge of endophytic fungi, and can help to the development of biocontrol techniques, which can solve the environmental friendly reduction of *Ambrosia artemisiifolia*.

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The molecular mechanism of sulfanilic acid biodegradation

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Sulfanilic acid (SA) is produced by the industry in large amount and – as a consequence of careless handling - it often appears in the wastes and environment. Because of its toxic properties, it should be eliminated from the natural milieu. Biodegradation is a natural environmentally sound solution for detoxification of our ecosystems.

Novosphingobium subarcticum SAI, a strain isolated from a contaminated industrial area, is a strictly aerobic chemoheterotrophic bacterium with astonishing metabolic versatility. Out of numerous aromatic compounds it can utilize sulfanilic acid as a sole carbon, nitrogen and sulfur source. Our previous studies identified the enzymes involved in the degradation of sulfanilic acid. The enzymes taking part in the